REMARKS

By present amendment the claims have been amended to present the claims in accordance with customary U.S. practice, care having been exercised to avoid any introduction of new matter.

The specification has been amended to include section headings in accordance with customary U.S. practice.

Claims 1-14, 18-19 and 22 have been canceled, and Claims 15-17, 20-21, and 23-24 have been amended as to form. Claims 25-46 have been added. Support for Claims 25-26 can be found in original Claims 20-21, respectively. Support for Claims 27-28 can be found in original Claims 4 and 15, support for Claims 29-30 can be found in original Claims 4 and 16, and support for Claims 31-32 can be found in original Claims 9 and 17. Support for Claims 33-34 can be found in original Claims 9, 18 and 22-23. Support for Claims 35-36 can be found in original Claims 5 and 9, and in the specification on page 19, lines 13-23, while support for Claims 37-40 can be found in original Claim 4 and in the specification on page 20, lines 4-19 and page 21, lines 4-18. Support for Claims 41 and 43 can be found in original Claim 4, support for Claim 45 can be found in original Claim 9, and support for Claims 42, 44 and 46 can be found in original Claims 13 and 14. Support for the claims may be found elsewhere throughout the specification. The amendments to the claims remove multiple dependencies and place the claims in United States form.

The amendments to the claims and the specification do not involve any introduction of new matter, whereby entry is believed to be in order and is respectively requested.

Attached is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version With Markings To Show Changes Made".

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

On page 1, after the title, was inserted:

--FIELD OF THE INVENTION--.

On page 1, line 8, was inserted:

--BACKGROUND OF THE INVENTION--.

On page 1, line 25, was inserted:

--DETAILED DESCRIPTION--.

In the Claims:

Claims 1-14, 18-19 and 22 have been canceled.

Claims 15-17, 20-21 and 23-24 have been amended as follows:

15. (Amended) A m[M]ethod for finding a chemical compound which binds to a polypeptide with the biological activity of a very long chain fatty acid elongase, comprising the [following] steps of:

a) contacting a polypeptide with the biological activity of a very long chain fatty acid elongase or a host cell containing [a] the polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and

b) determining the chemical compound which specifically binds to the polypeptide.

16. (Amended) A m[M]ethod for finding inhibitors and/or activators of a polypeptide with the biological activity of a very long chain fatty acid elongase, comprising the [following] steps of:

a) contacting a polypeptide with the biological activity of a very long chain fatty acid elongase or a host cell containing [a] the polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, [and]

b) determining whether the activity of the polypeptide is reduced or increased by the chemical compound and, where appropriate, and

c) determining the compound which specifically reduces or increases the activity of the polypeptide.

17. (Amended) A m[M]ethod for finding a compound which alters the expression of polypeptides with the biological activity of a very long chain fatty acid elongase, comprising the [following] steps of:

a) contacting a host cell containing a nucleic acid coding for a polypeptide with the biological activity of a very long chain fatty acid elongase with a chemical compound or a mixture of chemical compounds,

b) determining the polypeptide concentration, and

c) determining the compound which specifically influences the expression of the polypeptide.

20. (Amended) A m[M]odulator[s] of VLCFAE which are found by a method according to Claim 16 [or 17].

21. (Amended) A h[H]erbicidally active substance[s which are] found by a method according to Claim[s] 16 [or 17].

23. (Amended) An plant item selected from the group consisting of trangenic [Transgenic] plants, parts of plants, protoplasts, plant tissues [or] and plant propagation materials, [characterized in that, after introduction of a] comprising an introduced nucleic acid coding for a polypeptide having SEQ ID NO: 2, wherein the intracellular concentration of a polypeptide according to Claim 14 is increased or reduced compared with the corresponding wild-type cells.

24. (Amended) An plant item selected from the group consisting of plants [Plants], parts of plants, protoplasts, plant tissues or plant propagation materials, [characterized in that they contain] comprising a polypeptide having SEQ ID NO: 2 whose biological activity or expression pattern is altered by comparison with the corresponding endogenous polypeptides.

The following claims have been added:

--25. A modulator of VLCFAE which are found by a method according to Claim 17.

26. A herbicidally active substance found by a method according to Claim 17.

27. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,

d) sequences which have an identity of at least 60% with the sequences defined under a) to c),

e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,

f) sequences which have an identity of at least 60% with the sequences defined under e),

g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

h) sequences which have an identity of at least 60% with the sequences defined under g).

28. A method according to Claim 15, wherein the polypeptide comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2, and

d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

29. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,

d) sequences which have an identity of at least 60% with the sequences defined under a) to c),

e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,

f) sequences which have an identity of at least 60% with the sequences defined under e),

g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2, and

h) sequences which have an identity of at least 60% with the sequences defined under g).

30. A method according to Claim 16, wherein the polypeptide comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2, and

d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.

31. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

c) partial sequences at least 14 base-pairs long of the sequences

d) sequences which hybridize to the sequences defined under a) or b),

e) sequences which have an identity of at least 60% with the sequences defined under a) or b),

f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2

g) sequences which have an identity of at least 60% with the sequences defined under f),

h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

i) sequences which have an identity of at least 60% with the sequences defined under h),

j) sequences which are complementary to the sequences defined under a) to i), and

k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

32. A method according to Claim 17, nucleic acid comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

c) sequences which hybridize to the sequences defined under a) or b),

d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2

e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

f) sequences which are complementary to the sequences defined under a) to e), and

g) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to f)

33. A trangenic plant comprising a nucleic acid comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

c) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2

d) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

e) sequences which are complementary to the sequences defined under a) to d), and

f) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to e).

34. A trangenic plant according to Claim 33, comprising a nucleic acid comprises a sequence selected from the group consisting of:

a) the sequence shown in SEQ ID NO: 1, and

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2.

35. A method of determining with a target compound binds to a nucleic acid sequence coding a very long chain fatty acid elongase, comprising the step of contacting the target compound with a nucleic acid comprising a sequence selected form the group consisting of:

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

c) partial sequences at least 14 base-pairs long of the sequences defined under a) or b),

d) sequences which hybridize to the sequences defined under a) or

e) sequences which have an identity of at least 60% with the sequences defined under a) or b),

f) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2

g) sequences which have an identity of at least 60% with the sequences defined under f),

h) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

i) sequences which have an identity of at least 60% with the sequences defined under h),

j) sequences which are complementary to the sequences defined under a) to i), and

k) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to h).

36. A method according to Claim 35, wherein the nucleic acid comprising a sequence selected form the group consisting of:

a) the sequence shown in SEQ ID NO: 1,

b) sequences which code for a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2,

c) sequences which hybridize to the sequences defined under a) or b),

d) sequences which code for the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,

e) sequences which code for the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

f) sequences which are complementary to the sequences defined under a) to e), and

g) sequences which, because of the degeneracy of the genetic code, code for the same amino acid sequence as the sequences defined under a) to f).

37. A method of determining whether a target compound binds to a very long chain fatty acid elongase polypeptide, comprising the step of contacting the target compound with a polypeptide comprising a sequence selected form the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) partial sequences of the sequences defined under a) or b) which still have the biological activity of a VLCFAE,

d) sequences which have an identity of at least 60% with the sequences defined under a) to c),

e) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,

f) sequences which have an identity of at least 60% with the sequences defined under e),

g) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2,

h) sequences which have an identity of at least 60% with the sequences defined under g).

38. A method according to Claim 37, wherein the polypeptide comprises a sequence selected form the group consisting of:

a) the sequence shown in SEQ ID NO: 2,

b) sequences encoded by a nucleic acid having SEQ ID NO: 1,

c) sequences which include the C-terminally localized active site of the polypeptide shown in SEQ ID NO: 2,

d) sequences which include the specific N terminus of the polypeptide shown in SEQ ID NO: 2.

39. A method according to Claim 37, comprising the steps of :

a) providing a labelled substrate of the polypeptide, and

b) comparing the conversion of the labelled substrate incubated with the polypeptide in the presence of the target compound to the conversion of the labelled substrate incubated with the polypeptide in the absence of the target compound.

40. A method according to Claim 37, comprising the steps of :

a) providing a labelled ligand of the polypeptide, and

b) comparing the binding of the labelled ligand incubated with the polypeptide in the presence of the target compound to the binding of the labelled ligand substrate incubated with the polypeptide in the absence of the target compound.

41. A method according to Claim 15, comprising the step of contacting a host cell comprising a polypeptide of the sequence SEQ ID NO:2 with a chemical compound under conditions which permit the interaction of the chemical compound with the polypeptide.

42. A method according to Claim 41, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammaliam cells and plant cells.

43. A method according to Claim 16, comprising the step of contacting a host cell comprising a polypeptide of the sequence SEQ ID NO:2 with a chemical compound under conditions which permit the interaction of the chemical compound with the polypeptide.

44. A method according to Claim 43, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammaliam cells and plant cells.

45. A method according to Claim 17, wherein the host cell comprises a nucleic acid of the sequence SEQ ID NO:1.

46. A method according to Claim 45, wherein the host cell is selected from the group consisting of *E. coli* cells, yeast cells, insect cells, mammaliam cells